

RAW SEQUENCE LISTING

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Application Serial Number: 10|617,034A
Source: IFWO
Date Processed by STIC: 08|22|2005

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RAW SEQUENCE LISTING

DATE: 08/22/2005

PATENT APPLICATION: US/10/617,034A

TIME: 11:28:33

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Output Set: N:\CRF4\08222005\J617034A.raw

3 <110> APPLICANT: ITOH, NOBUYA
 4 WAKITA, RYUHEI
 6 <120> TITLE OF INVENTION: PROCESS FOR PRODUCING 3-HYDROXYCYCLOHEXANONE
 8 <130> FILE REFERENCE: Q76481
 10 <140> CURRENT APPLICATION NUMBER: 10/617,034A
 11 <141> CURRENT FILING DATE: 2003-07-11
 13 <150> PRIOR APPLICATION NUMBER: JP 2002-205207
 14 <151> PRIOR FILING DATE: 2002-07-15
 16 <160> NUMBER OF SEQ ID NOS: 15
 18 <170> SOFTWARE: PatentIn Ver. 3.2
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 348
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Corynebacterium pseudodiphtheriticum
 25 <400> SEQUENCE: 1
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 29 Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val
 30 20 25 30
 32 Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro
 33 35 40 45
 35 Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly
 36 50 55 60
 38 Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile
 39 65 70 75 80
 41 Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp
 42 85 90 95
 44 His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu
 45 100 105 110
 47 Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe
 48 115 120 125
 50 Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp
 51 130 135 140
 53 Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His
 54 145 150 155 160
 56 Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val
 57 165 170 175
 59 Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg
 60 180 185 190
 62 His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys
 63 195 200 205
 65 Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp
 66 210 215 220

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68 Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala
69 225      230      235      240
71 Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala
72      245      250      255
74 Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly
75      260      265      270
77 Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu
78      275      280      285
80 Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu
81      290      295      300
83 Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Ser Val Glu Thr
84 305      310      315      320
86 Phe Ser Leu Asp Asn Gly Ala Glu Ala Tyr Arg Arg Leu Ala Ala Gly
87      325      330      335
89 Thr Leu Ser Gly Arg Ala Val Val Val Pro Gly Leu
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93 <210> SEQ ID NO: 2
94 <211> LENGTH: 1047
95 <212> TYPE: DNA
96 <213> ORGANISM: Corynebacterium pseudodiphtheriticum
98 <220> FEATURE:
99 <221> NAME/KEY: CDS
100 <222> LOCATION: (1)..(1047)
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105 1      5      10      15
107 gag att ccc aaa ccc gag ccc ggt cca ggt gaa gtg ctc ctg gaa gtc 96
108 Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val
109      20      25      30
111 acc gct gct ggc gtc tgc cac tcg gac gac ttc atc atg agc ctg ccc 144
112 Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro
113      35      40      45
117 gaa gag cag tac acc tac ggc ctt ccg ctc acg ctc ggc cac gaa ggc 192
118 Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly
119      50      55      60
121 gca ggc aag gtc gcc gcc gtc ggc gag ggt gtc gaa ggt ctc gac atc 240
122 Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile
123 65      70      75      80
125 gga acc aat gtc gtc gtc tac ggg cct tgg ggt tgc ggc aac tgt tgg 288
126 Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp
127      85      90      95
129 cac tgc tca caa gga ctc gag aac tat tgc tct cgc gcc caa gaa ctc 336
130 His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu
131      100      105      110
133 gga atc aat cct ccc ggt ctc ggt gca ccc ggc gcg ttg gcc gag ttc 384
134 Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe
135      115      120      125
137 atg atc gtc gat tct cct cgc cac ctt gtc ccg atc ggt gac ctc gac 432

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138 Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp
139      130      135      140
141 ccg gtc aag acg gtg ccg ctg acc gac gcc ggt ctg acg ccg tat cac 480
142 Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His
143 145      150      155      160
145 gcg atc aag cgt tct ctg ccg aaa ctt cgc gga ggc tcg tac gcg gtt 528
146 Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val
147      165      170      175
149 gtc att ggt acc ggc ggt ctc ggc cac gtc gct att cag ctc ctc cgc 576
150 Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg
151      180      185      190
153 cac ctc tcg gcg gca acg gtc atc gct ttg gac gtg agc gcg gac aag 624
154 His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys
155      195      200      205
157 ctc gaa ctg gca acc aag gta ggc gct cac gaa gtg gtt ctg tcc gac 672
158 Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp
159      210      215      220
161 aag gac gcg gcc gag aac gtc cgc aag atc act gga agt caa ggc gcc 720
162 Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala
163 225      230      235      240
165 gca ttg gtt ctc gac ttc gtc ggc tac cag ccc acc atc gac acc gcg 768
166 Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala
167      245      250      255
169 atg gct gtc gcc ggc gtc gga tca gac gtc acg atc gtc ggg atc ggg 816
170 Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly
171      260      265      270
175 gac ggc cag gcc cac gcc aaa gtc ggg ttc ttc caa agt cct tac gag 864
176 Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu
177      275      280      285
179 gct tcg gtg aca gtc ccg tat tgg ggt gcc cgc aac gag ttg atc gaa 912
180 Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu
181      290      295      300
183 ttg atc gac ctc gcc cac gcc ggc atc ttc gac atc tcg gtg gag acc 960
184 Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Ser Val Glu Thr
185 305      310      315      320
187 ttc agt ctc gac aac ggt gcc gaa gcg tat cga cga ctg gct gcc gga 1008
188 Phe Ser Leu Asp Asn Gly Ala Glu Ala Tyr Arg Arg Leu Ala Ala Gly
189      325      330      335
191 acg ctc agc ggc cgt gcg gtt gtg gtc cct ggt ctg tag 1047
192 Thr Leu Ser Gly Arg Ala Val Val Pro Gly Leu
193      340      345
196 <210> SEQ ID NO: 3
197 <211> LENGTH: 325
198 <212> TYPE: PRT
199 <213> ORGANISM: Penicillium citrinum
201 <400> SEQUENCE: 3
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203 1 5 10 15
205 Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr

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206          20          25          30
208 Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
209          35          40          45
211 Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg
212          50          55          60
214 Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
215          65          70          75          80
217 Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
218          85          90          95
220 Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
221          100          105          110
223 Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
224          115          120          125
226 Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
227          130          135          140
229 Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
230          145          150          155          160
233 Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
234          165          170          175
236 Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
237          180          185          190
239 Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe
240          195          200          205
242 Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
243          210          215          220
245 Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
246          225          230          235          240
248 Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
249          245          250          255
251 Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
252          260          265          270
254 Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
255          275          280          285
257 Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
258          290          295          300
260 Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala
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263 Lys Asn Leu Ser Ala
264          325
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268 <211> LENGTH: 978
269 <212> TYPE: DNA
270 <213> ORGANISM: Penicillium citrinum
272 <220> FEATURE:
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274 <222> LOCATION: (1)..(978)
276 <400> SEQUENCE: 4
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279	1			5					10				15				
281	ggc	gtc	ggc	ttt	ggt	acc	ttc	gct	agt	gaa	ggt	tcc	aag	ggc	gag	acc	96
282	Gly	Val	Gly	Phe	Gly	Thr	Phe	Ala	Ser	Glu	Gly	Ser	Lys	Gly	Glu	Thr	
283				20					25				30				
285	tat	act	gct	gtc	acc	act	gcc	ctg	aag	acc	ggt	tac	cgt	cac	ttg	gac	144
286	Tyr	Thr	Ala	Val	Thr	Thr	Ala	Leu	Lys	Thr	Gly	Tyr	Arg	His	Leu	Asp	
287				35				40					45				
291	tgt	gcc	tgg	tac	tac	ctg	aac	gag	ggt	gag	gtt	ggt	gag	ggt	atc	cgt	192
292	Cys	Ala	Trp	Tyr	Tyr	Leu	Asn	Glu	Gly	Glu	Val	Gly	Glu	Gly	Ile	Arg	
293		50					55					60					
295	gac	ttc	ctg	aag	gag	aac	ccc	tcg	gtg	aag	cgt	gag	gac	atc	ttc	gtc	240
296	Asp	Phe	Leu	Lys	Glu	Asn	Pro	Ser	Val	Lys	Arg	Glu	Asp	Ile	Phe	Val	
297	65					70				75				80			
299	tgc	acc	aag	gtg	tgg	aac	cac	ctc	cac	cgt	tat	gag	gac	gtc	ctc	tgg	288
300	Cys	Thr	Lys	Val	Trp	Asn	His	Leu	His	Arg	Tyr	Glu	Asp	Val	Leu	Trp	
301					85				90				95				
303	tcc	att	gac	gac	tcc	ctg	aag	cgt	ctt	gga	ctt	gac	tac	gtt	gat	atg	336
304	Ser	Ile	Asp	Asp	Ser	Leu	Lys	Arg	Leu	Gly	Leu	Asp	Tyr	Val	Asp	Met	
305				100				105				110					
307	ttc	ctc	gtt	cac	tgg	ccc	att	gct	gcc	gag	aag	aat	ggc	cag	ggt	gag	384
308	Phe	Leu	Val	His	Trp	Pro	Ile	Ala	Ala	Glu	Lys	Asn	Gly	Gln	Gly	Glu	
309			115				120					125					
311	ccc	aag	att	ggc	cct	gac	ggc	aaa	tac	gtc	att	ctc	aag	gac	ctg	acc	432
312	Pro	Lys	Ile	Gly	Pro	Asp	Gly	Lys	Tyr	Val	Ile	Leu	Lys	Asp	Leu	Thr	
313		130				135				140							
315	gag	aac	ccc	gag	ccc	aca	tgg	cgc	gct	atg	gag	aag	att	tat	gag	gat	480
316	Glu	Asn	Pro	Glu	Pro	Thr	Trp	Arg	Ala	Met	Glu	Lys	Ile	Tyr	Glu	Asp	
317	145				150				155				160				
319	cgc	aag	gcc	agg	tcc	att	ggt	gtc	tcc	aac	tgg	acc	att	gcc	gac	ctt	528
320	Arg	Lys	Ala	Arg	Ser	Ile	Gly	Val	Ser	Asn	Trp	Thr	Ile	Ala	Asp	Leu	
321				165				170				175					
323	gag	aag	atg	tcc	aag	ttc	gcc	aag	gtc	atg	cct	cac	gcc	aac	cag	atc	576
324	Glu	Lys	Met	Ser	Lys	Phe	Ala	Lys	Val	Met	Pro	His	Ala	Asn	Gln	Ile	
325			180				185				190						
327	gag	att	cac	ccc	ttc	ctg	ccc	aac	gag	gag	ctg	gtg	cag	tac	tgc	ttc	624
328	Glu	Ile	His	Pro	Phe	Leu	Pro	Asn	Glu	Glu	Leu	Val	Gln	Tyr	Cys	Phe	
329			195				200				205						
331	tcc	aag	aac	att	atg	ccc	gtg	gcc	tac	tct	cct	ctg	ggc	tcg	cag	aac	672
332	Ser	Lys	Asn	Ile	Met	Pro	Val	Ala	Tyr	Ser	Pro	Leu	Gly	Ser	Gln	Asn	
333		210				215					220						
335	cag	gtt	ccc	acc	acc	ggt	gag	cgg	gtc	agc	gag	aac	aag	act	ctg	aac	720
336	Gln	Val	Pro	Thr	Thr	Gly	Glu	Arg	Val	Ser	Glu	Asn	Lys	Thr	Leu	Asn	
337	225				230				235				240				
339	gag	atc	gcc	gag	aag	ggc	ggc	aac	acc	ctt	gct	cag	gtt	ctt	att	gcc	768
340	Glu	Ile	Ala	Glu	Lys	Gly	Gly	Asn	Thr	Leu	Ala	Gln	Val	Leu	Ile	Ala	
341				245			250				255						
343	tgg	ggt	ctg	cgc	cgt	ggc	tac	gtc	gtt	ctc	ccc	aag	agc	tcc	aac	ccc	816
344	Trp	Gly	Leu	Arg	Arg	Gly	Tyr	Val	Val	Leu	Pro	Lys	Ser	Ser	Asn	Pro	
345				260			265				270						

VERIFICATION SUMMARY

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STATISTICS SUMMARY

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ha or Numeric or Xml: Numeric

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lication File Date: 07-11-2003

Unit: IFWO

tware Application: PatentIN3.2

al Number of Sequences: 15

al Nucleotides: 3043

al Amino Acids: 934

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